



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/727,898

DATE: 07/27/2004
TIME: 13:04:45

Input Set : N:\Crf3\RULE60\10727898.raw
Output Set: N:\CRF4\07272004\J727898.raw

SEQUENCE LISTING

- 1 (1) GENERAL INFORMATION:
 - 2 (i) APPLICANT: Williams, James A.
3 Thalley, Bruce S.
 - 4 (ii) TITLE OF INVENTION: Multivalent Vaccine For Clostridium
5 Botulinum Neurotoxin
 - 6 (iii) NUMBER OF SEQUENCES: 82
 - 7 (iv) CORRESPONDENCE ADDRESS:
 - 8 (A) ADDRESSEE: Medlen & Carroll
 - 9 (B) STREET: 220 Montgomery Street, Suite 2200
 - 10 (C) CITY: San Francisco
 - 11 (D) STATE: California
 - 12 (E) COUNTRY: United States of America
 - 13 (F) ZIP: 94104
 - 14 (v) COMPUTER READABLE FORM:
 - 15 (A) MEDIUM TYPE: Floppy disk
 - 16 (B) COMPUTER: IBM PC compatible
 - 17 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - 18 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 - 19 (vi) CURRENT APPLICATION DATA:
 - C--> 20 (A) APPLICATION NUMBER: US/10/727,898
 - C--> 21 (B) FILING DATE: 04-Dec-2003
 - 22 (C) CLASSIFICATION: 424
 - 23 (vii) PRIOR APPLICATION DATA:
 - 24 (A) APPLICATION NUMBER: US/08/704,159
 - 25 (B) FILING DATE:
 - 26 (viii) ATTORNEY/AGENT INFORMATION:
 - 27 (A) NAME: Ingolia, Diane E.
 - 28 (B) REGISTRATION NUMBER: 40,027
 - 29 (C) REFERENCE/DOCKET NUMBER: OPHD-02304
 - 30 (ix) TELECOMMUNICATION INFORMATION:
 - 31 (A) TELEPHONE: (415) 705-8410
 - 32 (B) TELEFAX: (415) 397-8338
 - 33 (2) INFORMATION FOR SEQ ID NO: 1:
 - 34 (i) SEQUENCE CHARACTERISTICS:
 - 35 (A) LENGTH: 24 base pairs
 - 36 (B) TYPE: nucleic acid
 - 37 (C) STRANDEDNESS: single
 - 38 (D) TOPOLOGY: linear
 - 39 (ii) MOLECULE TYPE: DNA (genomic)
 - 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 - 41 GGAAATTTAG CTGCAGCATC TGAC
 - 43 (2) INFORMATION FOR SEQ ID NO: 2:



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44      (i) SEQUENCE CHARACTERISTICS:
45          (A) LENGTH: 24 base pairs
46          (B) TYPE: nucleic acid
47          (C) STRANDEDNESS: single
48          (D) TOPOLOGY: linear
49      (ii) MOLECULE TYPE: DNA (genomic)
50      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
51 TCTAGCAAAT TCGTTGTGT TGAA          24
53 (2) INFORMATION FOR SEQ ID NO: 3:
54      (i) SEQUENCE CHARACTERISTICS:
55          (A) LENGTH: 20 base pairs
56          (B) TYPE: nucleic acid
57          (C) STRANDEDNESS: single
58          (D) TOPOLOGY: linear
59      (ii) MOLECULE TYPE: DNA (genomic)
60      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
61 CTCGCATATA GCATTAGACC          20
63 (2) INFORMATION FOR SEQ ID NO: 4:
64      (i) SEQUENCE CHARACTERISTICS:
65          (A) LENGTH: 19 base pairs
66          (B) TYPE: nucleic acid
67          (C) STRANDEDNESS: single
68          (D) TOPOLOGY: linear
69      (ii) MOLECULE TYPE: DNA (genomic)
70      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
71 CTATCTAGGC CTAAAGTAT          19
73 (2) INFORMATION FOR SEQ ID NO: 5:
74      (i) SEQUENCE CHARACTERISTICS:
75          (A) LENGTH: 8133 base pairs
76          (B) TYPE: nucleic acid
77          (C) STRANDEDNESS: single
78          (D) TOPOLOGY: linear
79      (ii) MOLECULE TYPE: DNA (genomic)
80      (ix) FEATURE:
81          (A) NAME/KEY: CDS
82          (B) LOCATION: 1..8130
83      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
84 ATG TCT TTA ATA TCT AAA GAA GAG TTA ATA AAA CTC GCA TAT AGC ATT          48
85 Met Ser Leu Ile Ser Lys Glu Glu Leu Ile Lys Leu Ala Tyr Ser Ile
86     1           5           10           15
87 AGA CCA AGA GAA AAT GAG TAT AAA ACT ATA CTA ACT AAT TTA GAC GAA          96
88 Arg Pro Arg Glu Asn Glu Tyr Lys Thr Ile Leu Thr Asn Leu Asp Glu
89     20           25           30
90 TAT AAT AAG TTA ACT ACA AAC AAT AAT GAA AAT AAA TAT TTG CAA TTA          144
91 Tyr Asn Lys Leu Thr Thr Asn Asn Glu Asn Lys Tyr Leu Gln Leu
92     35           40           45
93 AAA AAA CTA AAT GAA TCA ATT GAT GTT TTT ATG AAT AAA TAT AAA ACT          192
94 Lys Lys Leu Asn Glu Ser Ile Asp Val Phe Met Asn Lys Tyr Lys Thr
95     50           55           60

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96	TCA AGC AGA AAT AGA GCA CTC TCT AAT CTA AAA AAA GAT ATA TTA AAA	240
97	Ser Ser Arg Asn Arg Ala Leu Ser Asn Leu Lys Lys Asp Ile Leu Lys	
98	65 70 75 80	
99	GAA GTA ATT CTT ATT AAA AAT TCC AAT ACA AGC CCT GTA GAA AAA AAT	288
100	Glu Val Ile Leu Ile Lys Asn Ser Asn Thr Ser Pro Val Glu Lys Asn	
101	85 90 95	
102	TTA CAT TTT GTA TGG ATA GGT GGA GAA GTC AGT GAT ATT GCT CTT GAA	336
103	Leu His Phe Val Trp Ile Gly Gly Glu Val Ser Asp Ile Ala Leu Glu	
104	100 105 110	
105	TAC ATA AAA CAA TGG GCT GAT ATT AAT GCA GAA TAT AAT ATT AAA CTG	384
106	Tyr Ile Lys Gln Trp Ala Asp Ile Asn Ala Glu Tyr Asn Ile Lys Leu	
107	115 120 125	
108	TGG TAT GAT AGT GAA GCA TTC TTA GTA AAT ACA CTA AAA AAG GCT ATA	432
109	Trp Tyr Asp Ser Glu Ala Phe Leu Val Asn Thr Leu Lys Lys Ala Ile	
110	130 135 140	
111	GTT GAA TCT TCT ACC ACT GAA GCA TTA CAG CTA CTA GAG GAA GAG ATT	480
112	Val Glu Ser Ser Thr Thr Glu Ala Leu Gln Leu Leu Glu Glu Ile	
113	145 150 155 160	
114	CAA AAT CCT CAA TTT GAT AAT ATG AAA TTT TAC AAA AAA AGG ATG GAA	528
115	Gln Asn Pro Gln Phe Asp Asn Met Lys Phe Tyr Lys Lys Arg Met Glu	
116	165 170 175	
117	TTT ATA TAT GAT AGA CAA AAA AGG TTT ATA AAT TAT TAT AAA TCT CAA	576
118	Phe Ile Tyr Asp Arg Gln Lys Arg Phe Ile Asn Tyr Tyr Lys Ser Gln	
119	180 185 190	
120	ATC AAT AAA CCT ACA GTA CCT ACA ATA GAT GAT ATT ATA AAG TCT CAT	624
121	Ile Asn Lys Pro Thr Val Pro Thr Ile Asp Asp Ile Ile Lys Ser His	
122	195 200 205	
123	CTA GTA TCT GAA TAT AAT AGA GAT GAA ACT GTA TTA GAA TCA TAT AGA	672
124	Leu Val Ser Glu Tyr Asn Arg Asp Glu Thr Val Leu Glu Ser Tyr Arg	
125	210 215 220	
126	ACA AAT TCT TTG AGA AAA ATA AAT AGT AAT CAT GGG ATA GAT ATC AGG	720
127	Thr Asn Ser Leu Arg Lys Ile Asn Ser Asn His Gly Ile Asp Ile Arg	
128	225 230 235 240	
129	GCT AAT AGT TTG TTT ACA GAA CAA GAG TTA TTA AAT ATT TAT AGT CAG	768
130	Ala Asn Ser Leu Phe Thr Glu Gln Glu Leu Leu Asn Ile Tyr Ser Gln	
131	245 250 255	
132	GAG TTG TTA AAT CGT GGA AAT TTA GCT GCA GCA TCT GAC ATA GTA AGA	816
133	Glu Leu Leu Asn Arg Gly Asn Leu Ala Ala Ser Asp Ile Val Arg	
134	260 265 270	
135	TTA TTA GCC CTA AAA AAT TTT GGC GGA GTA TAT TTA GAT GTT GAT ATG	864
136	Leu Leu Ala Leu Lys Asn Phe Gly Gly Val Tyr Leu Asp Val Asp Met	
137	275 280 285	
138	CTT CCA GGT ATT CAC TCT GAT TTA TTT AAA ACA ATA TCT AGA CCT AGC	912
139	Leu Pro Gly Ile His Ser Asp Leu Phe Lys Thr Ile Ser Arg Pro Ser	
140	290 295 300	
141	TCT ATT GGA CTA GAC CGT TGG GAA ATG ATA AAA TTA GAG GCT ATT ATG	960
142	Ser Ile Gly Leu Asp Arg Trp Glu Met Ile Lys Leu Glu Ala Ile Met	
143	305 310 315 320	
144	AAG TAT AAA AAA TAT ATA AAT AAT TAT ACA TCA GAA AAC TTT GAT AAA	1008

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145	Lys	Tyr	Lys	Lys	Tyr	Ile	Asn	Asn	Tyr	Thr	Ser	Glu	Asn	Phe	Asp	Lys
146				325					330							335
147	CTT	GAT	CAA	CAA	TTA	AAA	GAT	AAT	TTT	AAA	CTC	ATT	ATA	GAA	AGT	AAA
148	Leu	Asp	Gln	Gln	Leu	Lys	Asp	Asn	Phe	Lys	Leu	Ile	Ile	Glu	Ser	Lys
149				340					345							350
150	AGT	GAA	AAA	TCT	GAG	ATA	TTT	TCT	AAA	TTA	GAA	AAT	TTA	AAT	GTA	TCT
151	Ser	Glu	Lys	Ser	Glu	Ile	Phe	Ser	Lys	Leu	Glu	Asn	Leu	Asn	Val	Ser
152				355					360							365
153	GAT	CTT	GAA	ATT	AAA	ATA	GCT	TTC	GCT	TTA	GGC	AGT	GTT	ATA	AAT	CAA
154	Asp	Leu	Glu	Ile	Lys	Ile	Ala	Phe	Ala	Leu	Gly	Ser	Val	Ile	Asn	Gln
155				370					375							380
156	GCC	TTG	ATA	TCA	AAA	CAA	GGT	TCA	TAT	CTT	ACT	AAC	CTA	GTA	ATA	GAA
157	Ala	Leu	Ile	Ser	Lys	Gln	Gly	Ser	Tyr	Leu	Thr	Asn	Leu	Val	Ile	Glu
158	385				390					395						400
159	CAA	GTA	AAA	AAT	AGA	TAT	CAA	TTT	TTA	AAC	CAA	CAC	CTT	AAC	CCA	GCC
160	Gln	Val	Lys	Asn	Arg	Tyr	Gln	Phe	Leu	Asn	Gln	His	Leu	Asn	Pro	Ala
161					405					410						415
162	ATA	GAG	TCT	GAT	AAT	AAC	TTC	ACA	GAT	ACT	ACT	AAA	ATT	TTT	CAT	GAT
163	Ile	Glu	Ser	Asp	Asn	Asn	Phe	Thr	Asp	Thr	Thr	Lys	Ile	Phe	His	Asp
164					420					425						430
165	TCA	TTA	TTT	AAT	TCA	GCT	ACC	GCA	GAA	AAC	TCT	ATG	TTT	TTA	ACA	AAA
166	Ser	Leu	Phe	Asn	Ser	Ala	Thr	Ala	Glu	Asn	Ser	Met	Phe	Leu	Thr	Lys
167					435				440							445
168	ATA	GCA	CCA	TAC	TTA	CAA	GTA	GGT	TTT	ATG	CCA	GAA	GCT	CGC	TCC	ACA
169	Ile	Ala	Pro	Tyr	Leu	Gln	Val	Gly	Phe	Met	Pro	Glu	Ala	Arg	Ser	Thr
170					450				455							460
171	ATA	AGT	TTA	AGT	GGT	CCA	GGA	GCT	TAT	GCG	TCA	GCT	TAC	TAT	GAT	TTC
172	Ile	Ser	Leu	Ser	Gly	Pro	Gly	Ala	Tyr	Ala	Ser	Ala	Tyr	Tyr	Asp	Phe
173	465				470					475						480
174	ATA	AAT	TTA	CAA	GAA	AAT	ACT	ATA	GAA	AAA	ACT	TTA	AAA	GCA	TCA	GAT
175	Ile	Asn	Leu	Gln	Glu	Asn	Thr	Ile	Glu	Lys	Thr	Leu	Lys	Ala	Ser	Asp
176					485				490							495
177	TTA	ATA	GAA	TTT	AAA	TTC	CCA	GAA	AAT	AAT	CTA	TCT	CAA	TTG	ACA	GAA
178	Leu	Ile	Glu	Phe	Lys	Phe	Pro	Glu	Asn	Asn	Leu	Ser	Gln	Leu	Thr	Glu
179					500				505							510
180	CAA	GAA	ATA	AAT	AGT	CTA	TGG	AGC	TTT	GAT	CAA	GCA	AGT	GCA	AAA	TAT
181	Gln	Glu	Ile	Asn	Ser	Leu	Trp	Ser	Phe	Asp	Gln	Ala	Ser	Ala	Lys	Tyr
182					515				520							525
183	CAA	TTT	GAG	AAA	TAT	GTA	AGA	GAT	TAT	ACT	GGT	GGA	TCT	CTT	TCT	GAA
184	Gln	Phe	Glu	Lys	Tyr	Val	Arg	Asp	Tyr	Thr	Gly	Gly	Ser	Leu	Ser	Glu
185					530				535							540
186	GAC	AAT	GGG	GTA	GAC	TTT	AAT	AAA	AAT	ACT	GCC	CTC	GAC	AAA	AAC	TAT
187	Asp	Asn	Gly	Val	Asp	Phe	Asn	Lys	Asn	Thr	Ala	Leu	Asp	Lys	Asn	Tyr
188	545				550					555						560
189	TTA	TTA	AAT	AAT	AAA	ATT	CCA	TCA	AAC	AAT	GTA	GAA	GAA	GCT	GGA	AGT
190	Leu	Leu	Asn	Asn	Lys	Ile	Pro	Ser	Asn	Asn	Val	Glu	Glu	Ala	Gly	Ser
191					565				570							575
192	AAA	AAT	TAT	GTT	CAT	TAT	ATC	ATA	CAG	TTA	CAA	GGA	GAT	GAT	ATA	AGT
193	Lys	Asn	Tyr	Val	His	Tyr	Ile	Ile	Gln	Leu	Gln	Gly	Asp	Asp	Ile	Ser

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194	580	585	590	
195	TAT GAA GCA ACA TGC AAT TTA TTT TCT AAA AAT CCT AAA AAT AGT ATT			1824
196	Tyr Glu Ala Thr Cys Asn Leu Phe Ser Lys Asn Pro Lys Asn Ser Ile			
197	595	600	605	
198	ATT ATA CAA CGA AAT ATG AAT GAA AGT GCA AAA AGC TAC TTT TTA AGT			1872
199	Ile Ile Gln Arg Asn Met Asn Glu Ser Ala Lys Ser Tyr Phe Leu Ser			
200	610	615	620	
201	GAT GAT GGA GAA TCT ATT TTA GAA TTA AAT AAA TAT AGG ATA CCT GAA			1920
202	Asp Asp Gly Glu Ser Ile Leu Glu Leu Asn Lys Tyr Arg Ile Pro Glu			
203	625	630	635	640
204	AGA TTA AAA AAT AAG GAA AAA GTA AAA GTA ACC TTT ATT GGA CAT GGT			1968
205	Arg Leu Lys Asn Lys Glu Lys Val Lys Val Thr Phe Ile Gly His Gly			
206	645	650	655	
207	AAA GAT GAA TTC AAC ACA AGC GAA TTT GCT AGA TTA AGT GTA GAT TCA			2016
208	Lys Asp Glu Phe Asn Thr Ser Glu Phe Ala Arg Leu Ser Val Asp Ser			
209	660	665	670	
210	CTT TCC AAT GAG ATA AGT TCA TTT TTA GAT ACC ATA AAA TTA GAT ATA			2064
211	Leu Ser Asn Glu Ile Ser Ser Phe Leu Asp Thr Ile Lys Leu Asp Ile			
212	675	680	685	
213	TCA CCT AAA AAT GTA GAA GTA AAC TTA CTT GGA TGT AAT ATG TTT AGT			2112
214	Ser Pro Lys Asn Val Glu Val Asn Leu Leu Gly Cys Asn Met Phe Ser			
215	690	695	700	
216	TAT GAT TTT AAT GTT GAA GAA ACT TAT CCT GGG AAG TTG CTA TTA AGT			2160
217	Tyr Asp Phe Asn Val Glu Glu Thr Tyr Pro Gly Lys Leu Leu Leu Ser			
218	705	710	715	720
219	ATT ATG GAC AAA ATT ACT TCC ACT TTA CCT GAT GTA AAT AAA AAT TCT			2208
220	Ile Met Asp Lys Ile Thr Ser Thr Leu Pro Asp Val Asn Lys Asn Ser			
221	725	730	735	
222	ATT ACT ATA GGA GCA AAT CAA TAT GAA GTA AGA ATT AAT AGT GAG GGA			2256
223	Ile Thr Ile Gly Ala Asn Gln Tyr Glu Val Arg Ile Asn Ser Glu Gly			
224	740	745	750	
225	AGA AAA GAA CTT CTG GCT CAC TCA GGT AAA TGG ATA AAT AAA GAA GAA			2304
226	Arg Lys Glu Leu Leu Ala His Ser Gly Lys Trp Ile Asn Lys Glu Glu			
227	755	760	765	
228	GCT ATT ATG AGC GAT TTA TCT AGT AAA GAA TAC ATT TTT TTT GAT TCT			2352
229	Ala Ile Met Ser Asp Leu Ser Ser Lys Glu Tyr Ile Phe Phe Asp Ser			
230	770	775	780	
231	ATA GAT AAT AAG CTA AAA GCA AAG TCC AAG AAT ATT CCA GGA TTA GCA			2400
232	Ile Asp Asn Lys Leu Lys Ala Lys Ser Lys Asn Ile Pro Gly Leu Ala			
233	785	790	795	800
234	TCA ATA TCA GAA GAT ATA AAA ACA TTA TTA CTT GAT GCA AGT GTT AGT			2448
235	Ser Ile Ser Glu Asp Ile Lys Thr Leu Leu Asp Ala Ser Val Ser			
236	805	810	815	
237	CCT GAT ACA AAA TTT ATT TTA AAT AAT CTT AAG CTT AAT ATT GAA TCT			2496
238	Pro Asp Thr Lys Phe Ile Leu Asn Asn Leu Lys Leu Asn Ile Glu Ser			
239	820	825	830	
240	TCT ATT GGG GAT TAC ATT TAT TAT GAA AAA TTA GAG CCT GTT AAA AAT			2544
241	Ser Ile Gly Asp Tyr Ile Tyr Tyr Glu Lys Leu Glu Pro Val Lys Asn			
242	835	840	845	

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10727898.raw

Output Set: N:\CRF4\07272004\J727898.raw

L:20 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:21 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:2911 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=32
L:7982 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=82